

1 GAACCCAGTT GCTTCAGCGA GTCGAAC TAC AGTTTAACC TCATCAAATA
51 TGGCATCTCC CTTGCTTGCT GCAGCAGGGA TGGAGAAAT GTCACTTCT
101 TTTTAAGCTA GCAAGCTTT TCTTTTCTT TTTCTTCTC TATTTAAAAA
151 TTCTAACATCAT GGATGCTTCT TCCGACCCCTT ATTCGCCTTA TGACGGGGGA
201 GGAGACAATA TTCCCCTGAG GGAATTACAT AAAAGAGGAA CTCATTATAC
251 AATGACAAAT GGAGGCAGCA TTAACAGTC TACACATTAA CTGGATCTT
301 TGGATGAACC AATTCCAGGT GTTGGTACAT ATGATGATT CCATACTATT
351 GATTGGGTGC GAGAAAAATG TAAAGACAGA GAAAGGCATA GACGGATCAA
401 CAGCAAAAAG AAAGAATCG CATGGGAAT GACAAAAAGT TTGTATGATG
451 CGTGGTCAGG ATGGCTAGTA GTAACACTAA CAGGATTGGC ATCAGGGCA
501 CTGGCCGGAT TAATAGACAT TGCTGCCAT TGATGACTG ACCTAAAGGA
551 GGGCATTGCGT CTTAGTGCCTG TGTTGGTACAA CCACGAACAG TGCTGTTGG
601 GATCTAATGA ACAACACATT GAAGAGAGGG ATAAATGTCC ACAGTGGAAA
651 ACATGGGCAG AATTAATCAT AGGTCAAGCA GAGGGTCTG GTTCTTATAT
701 CATGAAC TAC ATAATGTACA TCTTCTGGC CTTGAGTTTG GCCTTCTTG
751 CAGTTCCCT GGTAAAGGT TTTGCTCCAT ATGCCCTGTGG CTCTGGAATT
801 CCAGAGATTA AAACATTTTAAAGTGGATT CTCATCAGAG GTTACTTGGG
851 AAAATGGACT TTAATGATTA AAACCATCAC ATTAGTCCTG GCTGTGGCAT
901 CAGGTTGAG TTTAGGAAAA GAAGGTCCCC TGGTACATGT TGCCTGTTGC
951 TGCAGAAATA TCTTTTCCTA CCTCTTCCA AAGTATAGCA CAAACGAAGC
1001 TAAAAAAAGG GAGGTGCTAT CAGCTGCCCT AGCTGCAGGG GTTCTGTTAG
1051 CTGGTGTGC ACCAATTGGA GGAGTTCTT TTAGCCTGGA AGAGGTTAGC
1101 TATTATTTTC CTCTCAAAAC TTTATGGAGA TCATTTTTTG CTGCTTTAGT
1151 GGCTGCATTT GTTTTGAGGT CCATCAATCC ATTTGGTAAC AGCCGCTG
1201 TCCCTTTTTA TGTGGAGTAT CATAACCCAT GGTACCTTT TGAACTGTTT
1251 CCTTTTATTTC TTCTAGGGGT ATTTGGAGGG CTTTGGGGAG CCTTTTTCAT
1301 TAGGCAAAAT ATTGCCCTGGT GTCGTCGACG CAAGTCCACG AAATTTGAA
1351 AGTATCCCGT TCTGGAAGTC ATTATTGTTG CAGCCATTAC TGCTGTTGATA
1401 GCCTTCCCTA ATCCATACAC TAGGCTAAAC ACCAGTGAAC TGATCAAAGA
1451 GCTTTTACA GACTGTGGTC CCCTGGAATC CTCTTCTCT TGTA CACTACA
1501 GAAATGACAT GAATGGCAGT AAAATTGTCG ATGACATTCC TGATCGTCCA
1551 GCAGGCATTG GAGTATATTG AGCTATATGG CAGTTATGCC TGGCACTCAT
1601 ATTTAAAATC ATAATGACAG TATTCACTT TGCCATCAAG GTTCCATCAG
1651 GCTTGTTCAT CCCCAGCAGTG GCCATTGGAG CGATCGCAGG AAGGATTGTG
1701 GGGATTGCGG TGGAGCAGCT TGCCTACTAT CACCA CGACT GGT TATCTT
1751 TAAGGAGTGG TGTGAGGTG GGGCTGATTG CATTACACCT GGCCTTTATG
1801 CCATGGTTGG TGCTGCTGCA TGCTTAGGTG GTGTGACAAG AATGACTGTC
1851 TCCCTGGTGG TTATTGTTTG TGAGCTTA CACCGACT GAGGCTTGG AATATATTGT
1901 TCCCTTATG GCTGCAGTC TGACCAGTAA ATGGGTTGGA GATGCCTTG
1951 GCAGGGAAGG CATTATGAA GCACACATCC GATTAATGG ATACCCCTTC
2001 TTGGATGCAA AAGAAGAATT CACTCATACC ACCCTGGCTG CTGACGTTAT
2051 GAGACCTCGA AGGAATGATC CTCCCTTAGC TGTCCTGACA CAGGACAATA
2101 TGACAGTGGA TGATATAGAA AACATGATTA ATGAAACACAG CTACAATGGA
2151 TTTCCGTCA TAATGTCAA AGAATCTCAG AGATTAGTGG GATTTGCCCT
2201 CAGAAGAGAC CTGACAATTG CAATAGAAAG TGCCAGGAAA AAACAAGAAG
2251 GTATCGTTGG CAGTTCTCGG GTGTGTTTG CACAGCACAC CCCATCTCTT
2301 CCAGCAGAAA GTCCTCGGCC ATTGAAGCTT CGAAGCATTC TTGACATGAG
2351 CCCTTTACA GTGACAGACCA ACACCCCAAT GGAGATTGTG GTGGATATTT
2401 TCCGAAAGCT GGGACTGAGG CAGTGCCTTG TAACTCACAA TGGGCGCTC
2451 CTTGGCATTAA TAACAAAAAA AGATATCCTC CGGCATATGG CCCAGACGGC
2501 AAACCAAGAC CCCGCTTCAA TAATGTCAA CTGAATCTCA CAGATGAGGA
2551 GAGAGAAGAA ACGGAAGAGG AAGTTTATTG GTTGAATAGC ACAACTCTT
2601 AACCTGAGGG AGTCATCTAC TTTTTTTTCC TCCCTTACAA AAAAGAAAG
2651 GAAATATAAA AGCCGGGTTT TTGCAACATG GTTGCAAAAT AATGCTGGTG
2701 GAATGGAGGA GTTGTGTTGG GAGGGAAAGG AGAGAGAAGG AAAGGAGTGA
2751 GGTATTTCCC GTCTAACAGA AAGCAGCGTA TCAACTCCTA TTGTTCTGCA
2801 CTGGATGCAATCAGTGTGAGG ATGTGCTGTA TAGTGCAGGC TTGCGCCTCA
2851 ACAGAGATGA CAGCAGATC CTCGAGCACC TGGCCTGTTG CTCCAACATT
2901 GCAAAGACAC ATTACAGTC CCTATTCTA GAGGGATTAC TTTGAATTGA
2951 GCCATCTATA AACTGCAAG GTCTTGCCTT TTTTTTAAT CAAAAGTGT
3001 CTGTTTAATT CATGAATTGT ATAGTTAAGC ATTACCTTTC TACATTCCAG
3051 AAGAGCCTTT ATTCTCTCTC CTCTCTCTC CTCTCTACTG
3101 AGCTGTAACA AAGCCTCTT AAATCGGTGT ATCCTTTGAGCAGTCCTT

3151 TCTCATATTG AGATGTACTG TGATTTACT GAGGTTCAT CACAAGAAGG
3201 GAGTGTTC TGTGCCATTA ACCATGTAAT TTGTAACCATC ACTAAATGCT
3251 TGGAACAGTA CACATGCACC ACAACAAAGG CTCATCAAAC AGGTAAAGTC
3301 TCGAAGGAAG CGAGAACGAA ATCTCTCATT GTGTGCCGTG TGGCTCAAAA
3351 CCGAAAACAA TGAAGCTTGG TTTTAAAGGA TAAAGTTTTC TTTTTGTTT
3401 TCCTCTCAGA CTTTATGGAT AATGTGACCG GGTCTTATGC AAATTTCTA
3451 TTTCTAAAAC TACTACTATG ATATACAAGT GCTGTTGAGC ATAATTAAAT
3501 AAAATGCTGC TGCTTGACA GTAAAGAGAA AAAAAAAA AAAAAAAA
3551 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA
3601 AAAAAAAA AAAAAAAA AAAAAA (SEQ ID NO:1)

FEATURES:

5'UTR: 1-158
Start Codon: 159
Stop Codon: 2532
3'UTR: 2535

HOMOLOGOUS PROTEINS:**Top BLAST Hits:**

		Score	E
CRA 18000005109762	/altid=gi 2599548 /def=gb AAB95161.1 (AF029...	1575	0.0
CRA 18000005109763	/altid=gi 2599550 /def=gb AAB95162.1 (AF029...	1573	0.0
CRA 18000005227216	/altid=gi 4762023 /def=gb AAD29440.1 AF14277...	1572	0.0
CRA 18000004989660	/altid=gi 4502869 /def=ref NP_001820.1 chlo...	1570	0.0
CRA 18000005231972	/altid=gi 8134363 /def=sp Q9R279 CLC3_CAVPO ...	1561	0.0
CRA 18000004989700	/altid=gi 6680948 /def=ref NP_031737.1 chlo...	1560	0.0
CRA 18000004978791	/altid=gi 1705905 /def=sp P51792 CLC3_RAT CH...	1560	0.0
CRA 1000685681515	/altid=gi 6634696 /def=emb CAA71072.2 (Y0994...	1559	0.0
CRA 18000004989661	/altid=gi 1705903 /def=sp P51790 CLC3_HUMAN ...	1558	0.0
CRA 18000005226296	/altid=gi 4753144 /def=gb AAB88634.2 (U8346...	1556	0.0

EST:

	Score	E
gi 10993825 /dataset=dbest /taxon=96...	1562	0.0
gi 10934924 /dataset=dbest /taxon=96...	1336	0.0
gi 10952244 /dataset=dbest /taxon=96...	1251	0.0
gi 12383593 /dataset=dbest /taxon=96...	1205	0.0
gi 6591096 /dataset=dbest /taxon=9606 ...	1170	0.0
gi 10251711 /dataset=dbest /taxon=96...	1104	0.0
gi 2321385 /dataset=dbest /taxon=9606 ...	1045	0.0
gi 5594360 /dataset=dbest /taxon=9606 ...	975	0.0
gi 5422132 /dataset=dbest /taxon=9606 ...	965	0.0
gi 10327969 /dataset=dbest /taxon=96...	963	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:**library source:**

gi|10993825 Neuronal precursor cells-teratocarcinoma
gi|10934924 Whole embryo-mainly head
gi|10952244 Neuronal precursor cells-teratocarcinoma
gi|12383593 Small intestine-duodenal adenocarcinoma
gi|6591096 Lung-small cell carcinoma
gi|10251711 Breast-normal
gi|2321385 Schwannoma tumor
gi|5594360 Brain-tumor
gi|5422132 Testis
gi|10327969 Lung-large cell carcinoma

1 MDASSDPYLP YDGGGDNIPL RELHKGRTHY TMTNGGSINS STHLLDLLDE
51 PIPGVGTYDD FHTIDWVREK CKDRERHRRRI NSKKKESAWE MTKSLYDAWS
101 GWLVVTLTGL ASGALAGLID IAADWMTDLK EGICLSSALWY NHEQCCWGSN
151 ETTFEERDKC PWKWTWAELI IGQAEAEPSY IMNYIMYIFW ALSFAFLAVS
201 LVKVFAPYAC GSGIPEIKTI LSGFIIRGYL GKWTLMIKTI TLVLAVASGL
251 SLGKEGPLVH VACCCGNIFS YLFPKYSTNE AKKREVLSAA SAAGGSVAFG
301 APIGGVLFSL EEVSYYFPLK TLWRSFFAAL VAAFVLRIN PFGNSRLVLF
351 YVEYHTPWYL FELFPFILLG VFGGLWGAFF IRANIAWCRRKSTKFGKYP
401 VLEVIIVAAI TAVIAFPNPY TRLNTSELIK ELFDCGPLE SSSLCDYRND
451 MNASKIVDDI PDRPAGIGVY SAIWQLCLAI FKIIIMTVFT FGKVPAGLF
501 IPSMAIGAIA GRIVGIAVEQ LAYYHHDWFI FKEWCEVGAD CITPGLYAMV
551 GAAACLGGVT RMTVSLVVIV FELTGGLEYI VPLMAAVMTS KWVGDAFGRE
601 GIYEAHIRLN GYPFLDAKEE FTHTTLAADV MPRRRNDPPL AVLTQDNMTV
651 DDIENMINET SYNGFPVIMS KESQRLVGFALRRDLTIAIE SARKKQEGIV
701 GSSRVCFAQH TPSLPAESPR PLKLRSILDM SPFTVTDHTP MEIVVDIFRK
751 LGLRQCLVTH NGRLLGIIITK KDILRHMAQT ANQDPASIMF N (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 5

1	90-93	NETT
2	364-367	NTSE
3	392-395	NASK
4	587-590	NMTV
5	598-601	NETS

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 3

1	24-27	KKES
2	330-333	RRKS
3	331-334	RKST

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 8

1	22-24	SKK
2	333-335	STK
3	529-531	TSK
4	613-615	SQR
5	631-633	SAR
6	642-644	SSR
7	658-660	SPR
8	709-711	TKK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 13

1	27-30	SAWE
2	34-37	SLYD
3	92-95	TTFE
4	93-96	TFEE
5	105-108	TWAE
6	217-220	STNE
7	249-252	SLEE
8	383-386	SLCD
9	589-592	TVDD
10	666-669	SILD
11	674-677	TVTD
12	679-682	TPME
13	709-712	TKKD

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 18

1	49-54	GLASGA
2	53-58	GALAGL
3	72-77	GICLSA
4	88-93	GSNETT
5	189-194	GLSLGK
6	206-211	GNIFSY
7	234-239	GVSVAF
8	240-245	GAPIGG
9	245-250	GVLFSL
10	310-315	GVFGGL
11	313-318	GGLWGA
12	314-319	GLWGAF
13	408-413	GVYSAI
14	447-452	GAIAGR
15	491-496	GAAACL
16	541-546	GIYEAH
17	638-643	GIVGSS
18	692-697	GLRQCL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	99	119	1.810	Certain
2	182	202	2.131	Certain
3	233	253	1.398	Certain
4	256	276	1.019	Certain
5	290	310	1.770	Certain
6	321	341	0.797	Putative
7	361	381	2.093	Certain
8	400	420	1.539	Certain
9	473	493	1.739	Certain
10	496	516	1.218	Certain
11	540	560	1.568	Certain
12	570	590	0.975	Putative

BLAST Alignment to Top Hit:

>CRA|18000005109762 /altid=gi|2599548 /def=gb|AAB95161.1| (AF029346)
chloride channel protein 3 [Homo sapiens] /org=Homo
sapiens /taxon=9606 /dataset=nraa /length=818
Length = 818

Score = 1572 bits (4026), Expect = 0.0
Identities = 764/765 (99%), Positives = 764/765 (99%)

Query: 27 GTHYTMNGGSINSSTHLLDDEPIPGVGYDDFHTIDWVREKCKDRERHRRINSKKKE 86
GTHYTMNGGSINSSTHLLDDEPIPGVGYDDFHTIDWVREKCKDRERHRRINSKKKE
Sbjct: 54 GTHYTMNGGSINSSTHLLDDEPIPGVGYDDFHTIDWVREKCKDRERHRRINSKKKE 113

Query: 87 SAWEMTKSLYDAWSGLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSSLWYNHEQCC 146
SAWEMTKSLYDAWSGLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSSLWYNHEQCC
Sbjct: 114 SAWEMTKSLYDAWSGLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSSLWYNHEQCC 173

Query: 147 WGSNETTFEERDKCPQWKTWAELIIGQAEQPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 206
WGSNETTFEERDKCPQWKTWAELIIGQAEQPGSYIMNYIMYIFWALSFAFLAVSLVKVFA
Sbjct: 174 WGSNETTFEERDKCPQWKTWAELIIGQAEQPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 233

Query: 207 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCCG 266
PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCCG
Sbjct: 234 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCCG 293

Query: 267 NIFSYLFPKYSTNEAKKREVLSAASAAGVSAGVAPIGGVLFSLLEEVSYFPLKTLWRSF 326
NIFSYLFPKYSTNEAKKREVLSAASAAGVSAGVAPIGGVLFSLLEEVSYFPLKTLWRSF
Sbjct: 294 NIFSYLFPKYSTNEAKKREVLSAASAAGVSAGVAPIGGVLFSLLEEVSYFPLKTLWRSF 353

Query: 327 FAALVAAFVLRISINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA 386
FAALVAAFVLRISINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA
Sbjct: 354 FAALVAAFVLRISINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA 413

Query: 387 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 446
WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD
Sbjct: 414 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 473

Query: 447 YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGLFIPSMAI 506
YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGLFIPSMAI
Sbjct: 474 YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGLFIPSMAI 533

Query: 507 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSL 566
GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSL
Sbjct: 534 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSL 593

Query: 567 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTL 626
VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTL
Sbjct: 594 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTL 653

Query: 627 AADVMRPLRNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKECSRQLVGFALRRDLT 686
AADVMRP RNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKECSRQLVGFALRRDLT
Sbjct: 654 AADVMRPRRNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKECSRQLVGFALRRDLT 713

Query: 687 IAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPTVTDHTPMEIVVD 746
IAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPTVTDHTPMEIVVD
Sbjct: 714 IAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPTVTDHTPMEIVVD 773

Query: 747 IFRKLGLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN 791
IFRKLGRLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN
Sbjct: 774 IFRKLGLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN 818 (SEQ ID NO:4)

>CRA|18000004989660 /altid=gi|4502869 /def=ref|NP_001820.1| chloride
 channel 3; ClC-3 [Homo sapiens] /org=Homo sapiens
 /taxon=9606 /dataset=nraa /length=820
 Length = 820

Score = 1567 bits (4013), Expect = 0.0
 Identities = 764/767 (99%), Positives = 764/767 (99%), Gaps = 2/767 (0%)

Query: 27 GTHYMTNGGSINSSTHLLDEPIPGVGYDDFHTIDWVREKCKDRERHRRINSKKKE 86
 GTHYMTNGGSINSSTHLLDEPIPGVGYDDFHTIDWVREKCKDRERHRRINSKKKE
 Sbjct: 54 GTHYMTNGGSINSSTHLLDEPIPGVGYDDFHTIDWVREKCKDRERHRRINSKKKE 113

Query: 87 SAWEMTKSLYDAWSGLVVTLTGLASGALAGLIDIAADWMTDLKEGICLCLSALWYNHEQCC 146
 SAWEMTKSLYDAWSGLVVTLTGLASGALAGLIDIAADWMTDLKEGICLCLSALWYNHEQCC
 Sbjct: 114 SAWEMTKSLYDAWSGLVVTLTGLASGALAGLIDIAADWMTDLKEGICLCLSALWYNHEQCC 173

Query: 147 WGSNETTFEERDKCPQWKTWAELIIGQAEQPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 206
 WGSNETTFEERDKCPQWKTWAELIIGQAEQPGSYIMNYIMYIFWALSFAFLAVSLVKVFA
 Sbjct: 174 WGSNETTFEERDKCPQWKTWAELIIGQAEQPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 233

Query: 207 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCCG 266
 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCCG
 Sbjct: 234 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCCG 293

Query: 267 NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYFPLKTLWRSF 326
 NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYFPLKTLWRSF
 Sbjct: 294 NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYFPLKTLWRSF 353

Query: 327 FAALVAAFVLRISINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA 386
 FAALVAAFVLRISINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA
 Sbjct: 354 FAALVAAFVLRISINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA 413

Query: 387 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 446
 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD
 Sbjct: 414 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 473

Query: 447 YRNDMNAKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGLFIPSMAI 506
 YRNDMNAKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGLFIPSMAI
 Sbjct: 474 YRNDMNAKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIMTVFTFGIKVPSGLFIPSMAI 533

Query: 507 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSL 566
 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSL
 Sbjct: 534 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSL 593

Query: 567 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKE--EFTHT 624
 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKE EFTHT
 Sbjct: 594 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFEFTHT 653

Query: 625 TLAADVMPRLNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKECSRQLVGFALRRD 684
 TLAADVMPR RNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKECSRQLVGFALRRD
 Sbjct: 654 TLAADVMPRRNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKECSRQLVGFALRRD 713

Query: 685 LTIAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPFTVTDHTPMEIV 744
 LTIAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPFTVTDHTPMEIV
 Sbjct: 714 LTIAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPFTVTDHTPMEIV 773

Query: 745 VDIFRKLGRLQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN 791
 VDIFRKLGRLQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN
 Sbjct: 774 VDIFRKLGRLQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN 820 (SEQ ID NO:5)

>CRA|1000685681515 /altid=gi|6634696 /def=emb|CAA71072.2| (Y09941)
 putative chloride channel ClC-3 [Xenopus laevis]
 /org=Xenopus laevis /taxon=8355 /dataset=nraa
 /length=791
 Length = 791

 Score = 1559 bits (3993), Expect = 0.0
 Identities = 745/791 (94%), Positives = 771/791 (97%)

 Query: 1 MDASSDPYLPYDGGGDNIPLRELHKRGTHYTMTNGGSINSSTHLLDLLDEPIPGVGTYDD 60
 MD SSDPYLPYDGGGDNIPLR+LHKRGTHYT+TNGG+INS+THLLDLLDEPIPGVGTYDD
 Sbjct: 1 MDISSLDPYLPYDGGGDNIPLRDLHKRGTHYTNTNGGAINSTTHLLDLLDEPIPGVGTYDD 60
 (SEQ ID NO:6)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
CE00039	CE00039 chloride_channel	1671.9	0	1
CE00420	E00420 CLC	1288.1	0	2
PF00654	Voltage gated chloride channels	1172.4	0	1
PF00571	CBS domain	78.1	7e-20	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00654	1/1	71	622 ..	1	621 [.]	1172.4	0
PF00571	1/2	645	690 ..	11	54 .]	31.4	5.8e-07
CE00420	1/2	32	697 ..	1	729 [.]	1174.4	0
PF00571	2/2	726	778 ..	1	54 [.]	47.4	2.2e-11
CE00420	2/2	722	791 .]	867	942 ..	110.6	6.5e-32
CE00039	1/1	60	791 .]	1	804 [.]	1671.9	0

1 AATTCTATAAC AAATATAATT ATATAGATAT ATATTACATA TACACACAAT
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57251 TGTGTAATAT TGTTGATTA AATGATGGCA CCGACTTCAT TAAGTTAAA
57301 AACTCAGTAC TAGTTAAATG GGGCAACTTT TCATAAAGCT TTGCTAGTCC
57351 TTGAGCCCTT TTATTTGTTA AATGGCTCAA CTGGAACCTA AGCTGAGTTG
57401 TTACAAACTA TTATTTGCTT CAAGTTGTT TCTGTTCTG GCATGGCTT
57451 TTCTTTGTG TACTGACAAA TATAATGTT ATTCTGTTGA GTTATGGTTA
57501 ACTATGAACA CAGAACTGTG AGGGATTAAT TTTCATATTT CAGTTTGTG
57551 ATTAATTCCC AGGTATTTGG CAGCAGAT ATTAGAAAGG AAAATATTTA
57601 AAAGAAAGTG TAAAAATAAC GAAGTGTATA GAGCGAGGGG TGGATAGCTA
57651 ATTAAAATTT TGTCTGGTCC TGCCCTGTTCA TATGAAAAAA GGGGTTGGAC
57701 TTTCTTCTAA GGGAAATATAT TAAATTGTT TCATCATATT TTCCCTATTT
57751 CTGTCGTCA AGGAAATAA ATTGATACAT ATATGGGGAG AAAAGAGATC
57801 ATTTAGGGAA GTGGCTCATG GGACTTTTG TTTTGTGTTA AGTGTATTAG
57851 GAAGTCGGGT GTTTTTTTTC TCACCTAAAT TATTTAAAAC CCAGAAAAGA
57901 AATGATATCT TCTGGTTTT AAAGGAGACC ATGAAGTTCT GCATAGCTAT
57951 CATTGATGTG TAGTCATAC TGCATTTTA GAAGTGGAAA ATAGTTATTT
58001 GGAGGAAGAT AACAAATCTG GAACCTTAGG TGCAAGGAGA AAAAGAATAG
58051 ATGAAAGGGA AAGATGTTTG TAAATTATAA AAATTCAT TAGCTATTGG
58101 TTTCTGCAC TTTATATTTT AACTGCAGAA TTTTCAAAA TCAGTTAAC
58151 TTGGTGAAT TAGCAGGATG TTAATAGGAG TGACTCAGAA AAAAACATTT
58201 TGTGACTGTC TAAGTTGGA AAGTATGGA TAAATACAA TTGAGGTTTC
58251 TTTACTATGG AACTCCTCA GACTTATAAT ATGTTGATAT TCTTTGATT
58301 CCAGATGAGG GGATGGGTAA TAGGATACAT GGTGTTCCAG ACTTGTGTTGA
58351 AAATGCAACT ATTTTGGGTG TGCAGGGAAAG GATATAGTAG AACTCATGGG
58401 AACTGGTGTG TCTTGGAAAC TGCTTGGAA ATGCTGGGTT ATGCCCTGTT
58451 AACTCTTACA TCATTAGTT TTAGCCCCAA AGGAAACAGC AAATAATGTT
58501 TTATATGAGC CACATTTGCG TTGATTTCCTT CTTCCACTCT GTAAAATTAC
58551 TAAAGCAGCA CTCTGACTTT ATTATGCTCA AATCGCTCTT CTCCATTAAT
58601 GTGTGTTTCT CCATCTTTA GGGTTTTAC TTATATAATA CAGAGATTAC
58651 TGTGAAAAT TCTAAATTG CCACTGGTC GTTATACATT TGTAACCTTC
58701 CTCACAGTAT ATTTTGTGAT TTGGCAGAGT TTACCAATAT AGATGATACT
58751 AACTGAAATT AATCATTCTG TATAATTGGA TAGAAAAGCA TGAGTAAGAA
58801 TTCAATTGGT ATTATATTTA ATTAATTGCC AAGATTTCA CATTTCCTGA
58851 CTACAACAAT AAAATCAAAT GAATTGATGG CTTAAAAAAA AGAAATCTCA
58901 AATGTTAGT CAATGAAGAA CATCTATTGA ATGAGTGAAT GTTCATTATA
58951 TATAGTGCAT TTTCTGAGCT TTTTGGAGG GGGAAAGTTGC TCCCATGCTC
59001 TGAGAACTTT TAAGGATCGA TACATTATTT TTAACATAAT AATGAGAAAA
59051 CATGAGCAGA GAACCCATT CTGTCATTCC CATTCTCTAT CCTCCTGCTC
59101 CCCCACCTCC CACCCCCAGCC ATCAAGCTAA GTAACATTATT TACACCTGGA
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59401 TAGCAATCTA ATTATTTCA TGTATCCTCA TTATGAGAAT TTATGTCCAT
59451 CACTTGCTT GATGTGATAA CAGTGACATG CTTAAATGAGA AACAAATTGTT
59501 ATTTAGAAAA AAATGCACAA AGTGAAGTC CTTTAATCC CTAATCATAA
59551 ATACATTCTA TTAGCTTACT TTAAGAAGTG GCAGTCACAG CTCCTGAACA
59601 TTAGGGAGTG TTTCTTTGG TCAGCATTAT TTATTTAGTG CACATTGCCT
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59751 CTGTTGTTGTG ACATCATAGA AATTAGAAAA ATATTTCTT CTGAGGAAAG
59801 AACATTGTAA ATGAAACTCT ACATATCAGA GGTCTATAGC TATGTATCAA

59851 TATTAAGTTT CTTTTGACT TTGCTTGTA GTCATCTTC A TTCCAAACTT
59901 TCATAATTAT TATTTTTACT TTAAAAAGAA AAATAACCCA CCAATATTGA
59951 AGATTAGTAT TGTGTCACTT TTGAAAGTCA GTAGAATTAA TGCAAAAGGA
60001 ACCTGGAAC TTAAATCATT TTGTTTTAT TTCTAAAGT TCATGAGACT
60051 CATTCTTATG GTTCATGTT TTATTTTTCTC TCTCATTCTT TATCATTATG
60101 ATTGGAAACT CTTTTAATT AATTCTCAG ACAGTTATTA GCATAATAAT
60151 CTGTTTCAGG ATTGTCCTGG GGATCATCAC AAAGAAGAAC ATATTAGAGC
60201 ATCTCGAGCA ACTAAAGCAG CACGTCGAAC CCTTGGGTGAT TAGATATATC
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60301 CTGTTGAGTT CTGTCCTTCC CAGATATCTG CTGAACAAAA ATATCCTACT
60351 ATGCTGCCAA TTACATTGT ATCTGATAAA ATGTGTCGT AAGATAAATT
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60451 CTCATCAAAT CATTCAATTAC AATTTCAGAA CTGTAACACAG TTTGGTAGTG
60501 GAATAAGTGA ATATTATTGG ACATTCTTAA AGTGAATATG GCAAATCTGT
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60601 GTCTGACCCA TCCCCGCAAG CCCCCCTTTT TTTTTTTAAA TGTTCCCGA
60651 TCTTGTGGTA GTCTTATGGT AAATCTAACG TCCTAAAGGA TTTTAAAGGA
60701 GCTTAGCAAT TAGAACTGCT TACAGTTAAA TGAGTTTTT AATGGGCACA
60751 CTAACTAGAG TGTAATGTGT ATATTATTG TGATCATAGC ATTGTTCTT
60801 TTTCTGCTAT ACCCTGCATA TCTTCAAAGT CACAGTGTGT GTCCTGCCAT
60851 CTCATTAGTG AATTGTACCT AGATTATGTG TGTGCCCTT TTGTATGATG
60901 TTTCTGGAAC GCTATAAGCA GCTTTAGAG TCAAATGCAT TCATTTAAC
60951 TGGCTTTATG TCCTAGTGGT TTCATGACTA CAAATTGAA TTATCTTACT
61001 GCATAACATA AAAATGTCT GGCTTAGCA ATTAATGCC GAAATTATTT
61051 TGCCCTGCAA TTGTCATACC TGTATGAAAC CTGTCGGAGT TTGCTTAAGT
61101 GCACAACGTAA TTATGTATTCT CTGTTGTAT GCTAATATTT CACAAGTGT
61151 TCATGCATCC TTTTTAAAAAA AACTACTAAC CAGAATATTA TCGTAGCTAC
61201 TCATTCATTC TGCTTTCTGC TTCACCTATA ATAATCTTTT AGGACTGCC
61251 TCTGATTTT CACCTATCTT TTAATGTAAG CATTAAACAC TAAGACTTTC
61301 ATAAAAGCAC TGTATCTTAA CTTTCCTGGC CTAATCAAA AAAAGGAAAA
61351 CATTGATAAG TGTCTTAGAA ACTTGGATTCT TTGTTATAGAT TTGTTCTGG
61401 GGCTCTGATG TTTGGGATTG ACGTTCTGTG CTGACCATT TATATGCATT
61451 TTATCTTAAT AGTATGTGT TTCATGAAGA TTCTGATACA AGTGGGCAAT
61501 CCTTAAATTAA TCTTGGAAA ATTGGTTAAT TTGGTTAAA AAAGGGAAAG
61551 TGGCTGGGTG CAGTGGCTCA CGCCTGTAAT CCCCAGCACT TTGGGAGGCC
61601 GGGACGGGTG GATCACAAGG TCAGGAGTTG AAGCCCATT TGGCCAACAT
61651 GGTGAAACCC TGTCTCTACT GAAAATAATT GGGGCATGGT GGCACATGCC
61701 TGTAATCCCA GCTACTTGGG AAGCTGAGGC AGGAGAATTG CTTGAACCGG
61751 GGACCCAGGA GGCAGGAGTTG CAGTGAGCT GAGATCGCGC CACTGCACTC
61801 CAGCTGGGC TACAGAGCGA GACTCTGTCT CAAAAAATAA ATAAATAAT
61851 AAATGAAAAA GAGAAAATAT TGAGAGGATT TGTCATCAT TTTACTGCTC
61901 TCTTCATGTG ATGGAAATCA ATTTCTTC TCAAATGGGA TCAGTATCAT
61951 TTCCTAGTCA TACATCCATC CAGTTTTGT TACTTTTTG TTGGCATAACA
62001 TTAATCAAAA TAGCTCTGCT TCATTGAGGC ATGCAGTCCT CAGACTCTCG
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62101 GGATGGTTGC TGGATAATTAA TAATATCTTT ACCAATAAAG TACTTTTGG
62151 AAATACAAAAA TCAGGCTGCT TGCTTGTCT TATTCTGTCA AACAAAAGG
62201 ATTTAGCTAT AGATTTAGCT TCTCCTTTA TTTTCCCTTT TATTCATAG
62251 GAGTCTTCTG TTATTCCTT TCAGGCGCCT CCTTGGCATT ATAACAAAAA
62301 AAGATATCCT CCGGCATATG GCCCAGACGG CAAACCAAGA CCCCCTCTCA
62351 ATAATGTTCA ACTGAATCTC ACAGATGAGG AGAGAGAAGA AACGGAAGAG
62401 GAAGTTTATT TGTTGAATAG CACAACCTT TAACCTGAGG GAGTCATCTA
62451 CTTTTTTTCTC CTCTTTACA AAAAAAGAAA GGAAATATAA AAGCCGGTT
62501 TTTGCAACAT GTTTGCAAA TAATGCTGT GGAATGGAGG AGTTGTTGG
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62601 AAAGCAGCGT ATCAACTCCTT ATTGTTCTGC ACTGGATGCA TTCACTGAG
62651 GATGTCCTG ATAGTGCAGG CTTGCGCCTC AACAGAGATG ACAGCAGAGT
62701 CCTCGAGCAC CTGGCCTGTT GCTCCAACAT TGCAAAGACA CATTATCAGT
62751 CCCTATTCTC AGAGGGATTAA CTTTGAATTG AGCCATCTAT AAAACTGCAA
62801 GGTCTTGGCC TTTTTTTAA TCAAAACTGT TCTGTTTAAT TCATGAATTG
62851 TATAGTTAAG CATTACCTT CTACATTCCA GAAGAGCCTT TATTTCTCTC
62901 TCTCTCTCTC TCTCTCTCTC TCTCTCTACT GAGCTGTAAC AAAGCCTCTT
62951 TAAATCGGTG TATCCTTTTG AAGCAGTCCT TTCTCATATT GAGATGTACT

63001 GTGATTTAC TGAGGTTCA TCACAAGAAG GGAGTGTTC TTGTGCCATT
63051 AACCATGTA TTTGTACCAT CACTAAATGC TTGGAACAGT ACACATGCAC
63101 CACAACAAAG GCTCATCAA CAGGTAAAGT CTCGAAGGAA GCGAGAACGA
63151 AATCTCTCAT TGTGTGCCGT GTGGCTCAA ACCGAAAACA ATGAAGCTTG
63201 GTTTAAAGG ATAAAGTTT CTTTTTGTT TTCTCTCAG ACTTTATGGA
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63551 ATATTTTAT GGATTAATTA CAGATCAGTT AATATTGCAC
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63651 ACAAAATACAG AGATATGAAC AAAGTTACA GTGGGAACAA AGGTTAAAAA
63701 AAAGGTTGTG GTTCTCTCTC TGTGATCCAG TGTGCACATA AACCTTTCTC
63751 TGATCTTCA CTGCCATCCT CTGGATTATG TCTTCTGACC TGTCCATT
63801 GACCCATTAA CTGGAAAGTT GAAAAACTAC ATTAACGTGA AAGTTGAAAA
63851 ACTACATTAC TTTGGAGAA AAAACCGAAA GTTCTGTAT ACCTCTTAA
63901 AAAAAAAATC AAACCAAAAAA TGTAACAAAC ATAGAATTGC AAAGATAGCA
63951 GTTAAAATTT TAATCTGAAA ATAACCTTTG AATCTCGGGC TAGGTTATGT
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64051 TAAAATGCAC TGGATTATAT TTGGGATT TTGGGTTGGA ATTGTCTGTT
64101 TTAATCACAG CCTTAATTCA CAATTGGCAA AGGCAGTTA CTCAAAGGAC
64151 TGGCTAAAT ATTCTGTAAT TATGCATT TGATAGGAAA ATGAAATT
64201 TGAAACAGA CATTCTCTT TTTTTGGCT GGAGTGCAGT GGGGCATGGT
64251 CTTGGCTCAC TGCAGCGTTG ACCACCTGGG CTCAGTGAT ACTCCGCCT
64301 CAGCCACCCA AGTAGCTGGC ACTACGGCA CACGCCACCA TGCCCAGCTA
64351 ATTTTTTGT ATTTTTAGTA GAGATGGGT TTTGCCATGC TGCCCAGGCT
64401 GGTCTCAACT CCTCAGCTCA AGCAACTCTGC CTGCGTGAGC CTCCCAAAGT
64451 GGTGGAATTA CAGGCGTGGG CCACTGCGCC TGGCCAGAC AGACATT
64501 TGAAACACAA CTGGCAATGA GCTGTTTTA CATTGAAA GTGATTCTC
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64601 AAGACATAAG ATCATGAAGC CATATAAGAA TGAGGATTGA AAGTTGAGCA
64651 AAATTTCCGG GATTTGGGA AACATTCTTA GCTGTCGTAT CTGCCTAAA
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64751 CCCTTCAAA GTTTTTGAG CCATCCAGAG TAAATCATT TCTAAATGAT
64801 AGTTCTGTAT ATCTCCAAGT CGTCTTAAGT GTATTTGCCT GTGTGCAACG
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64901 CCTGAGTTAA TAGCCTTCAA AGGACAAATC GTTTCTTTG CAGATAGCTT
64951 CGTAAAACCTT CACATGGAGT TTATTTTATC ATATTCCTCCT TTTTTATTTC
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65051 GGATATTAAT TAAAGCTTA ATTTGTTTT TTGGTATATT TCTATCCCTA
65101 GTATTTCTAT CTTACTGCTA AAATACAGGA AAAAGTGCCTG ATTTTTAATG
65151 CATTAGTGG TTTTCTTTGG TGTTATCTGT TCCATTTTC TTTTTCATAC
65201 ATTGAAGTGT GTCTCCTTT CAACCAAAAT AATGAAATAG TGGAGACCAT
65251 GAAATTGTTG TGCCTGGCTA ATTGGCAAAT TAATTTACCA ATATAATAAG
65301 TGTAGCGCCT TGTGTTGAATA CCCTTTGAA GAAGGTATGA TGAGAATGGG
65351 CAAGGGTGT (SEQ ID NO:3)

FEATURES:

Start: 2159
Exon: 2159-2237
Intron: 2238-22041
Exon: 22042-22199
Intron: 22200-30359
Exon: 30360-30459
Intron: 30460-31475
Exon: 31476-31663
Intron: 31664-32964
Exon: 32965-33087
Intron: 33088-34548
Exon: 34549-34755

Intron: 34756-37975
 Exon: 37976-38056
 Intron: 38057-39552
 Exon: 39553-40098
 Intron: 40099-46366
 Exon: 46367-46553
 Intron: 46554-49237
 Exon: 49238-49636
 Intron: 49637-55445
 Exon: 55446-55662
 Intron: 55663-62274
 Exon: 62275-62362
 Stop: 62363

CHROMOSOME MAP POSITION:

Chromosome 4

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
1275	T	C	Beyond ORF(5')
1456	T	C	Beyond ORF(5')
5893	G	A	Intron
6226	A	G	Intron
8866	T	G	Intron
10397	C	T	Intron
10621	T	-	Intron
19651	A	G T	Intron
19891	T	-	Intron
20272	C	A	Intron
20412	T	A	Intron
23340	A	G	Intron
29948	T	A	Intron
33579	A	C	Intron
40762	G	A	Intron
40936	T	C	Intron
45998	A	G	Intron
47771	T	C	Intron
48117	C	T	Intron
54563	T	G	Intron
58735	C	T	Intron
59643	C	A	Intron
61638	G	T	Intron
63291	G	C	Beyond ORF(3')
63463	A	G	Beyond ORF(3')
63636	G	A	Beyond ORF(3')
63998	T	C	Beyond ORF(3')

Context:

DNA

Position

1275 GCATTTCAGGAGGAGAATCTCCAGTCTAGAGGAATCCTCTCAGAGGTAGCTATAAAATA
 TTGAACCTGATCTTCAATAAGCATTGTGCGGTTTTGTTTTGTTTTAATGACAGTTT
 TAAACAAGAAAGTTGCTTTATTTCTGAACCTTCATAAAAATTTCTATTAAAGAGACAATTT
 CTGAATTTATAACAATTCTAGAACAGTTGAGTACCTCACTTTGAGACACATTTGCT
 AAAAGTTAAAACACAAAACCCTTATGAGATAAAATAGGAAGCTAGTAGAGATAGGAAAG
 [T, C]
 CCTCTGCTTAGTAAACCTTTTGCCTAGTTAGACACATACAATAGTAAAGTTACTT
 AGTACGTTGATAGTTCTTCTCCTCAAAAGCTACAATGTCTTACTAGCTAGTTCCCTC
 AAGAAAGGAAACAAGAAGCCGCTGGAGGAGATTGGTAGTGGGATAAAACACTATTCAAC

	TCTTCAGTTATCGGTTTAAATCCTCAATGAAAGGCTGCTGTATTATAGAGTATTTT TTTTTATTTTAATAGACTTAGAACCAAGTTCTGAGAAACCTTGGCATATTGTAGTT
1456	TGAATTATTAACAATTCTAGAACAGTTGAGTACCTCACTTGAGACACATTTGCTA AAAGTTAAAAACACAAACCCCTATGAGATAAAATAGGAAGCTAGTAGAGATAGGAAAGT CCTCTGCTTAGTAAACCTCTTTTGCCTAGTTAGACACATACAATAGTAAAGTACTT AGTACGTTGATAGTTCTTCTCTAAAGCTACAATGTCTACTAGCTAGTCCCTC AAGAAAGGAAACAAGAACGCGCTGGAGGAGATTGGTAGTGGATAAAACACTATTCAAC [T, C] CTTCAGTTATCGGTTTAAATCCTCAATGAAAGGCTGCTGTATTATAGAGTATTTT TTTTTATTTTAATAGACTTAGAACCAAGTTCTGAGAAACCTTGGCATATTGTAGTT TTTTATGGCTATGACTCACATGACATTACTGTATAAAACTAGTACATTCTCGTAAAC CACACAAACTACTAGAGTGCTCTCATTTTCTACATTAGAAATGAAAAGGGCATT GTCTGCATTCAAATTCTCTTTACATCTCTGTATTACTTTCCCTTATATTATC
5893	TCTAGTTGACAAGACTGAGGTAAAGGAATTGTTAAGGAAAAGTCAGAATTCCATCCAGATA TTTGGCTCATACTTTAATCATGAGGCTAAACTGCTTCTCTACACGTATCTTCATAGTA ACTTGTGTTTAAGTCTGGTAGAACGATAAGAAGTTAAACACAGACAGAACCTGTGGA AGTTAGTAAATTCTAGTGAACGATAGAAATGATAGAAATCTCTTCCCCAAAGTCC CAAGAACAGATTAGTCTGCTTGACAAGTGTATCAAAGTAGACTGTTCTCACACAC [G, A] GGGGACTCAATAGGGCATTCTGGTGGATATAATAAAATGAGTAAATGCGATAACAGGAG GAAATGCCTAGTGTGCTCTGGATTAGTTGATAACAACAAAGGCAGCTTGTG AGTCAGTAGAGAGGGTAGTGTAGAAAGGTGGAAGTGGAGTGGCAGATCCTAGAGGA CTAATGATGGCTTAACCACAAAAAGTCGCTTGCATTGAA
6226	ATAAAATGAGTAAATGCGATAACAGGAGGAATGCCTAGTGTGTTGCTCTGGATTAGTT TTGATACAACAAAGGCAGTTGTTGTGAGTCAGTAGAGAGGGTAGTGTAGAAAGGTGGA AGTTGGAAGAGTGGCAGATCCTAGAGGACTAATGATGGCTAAACACAAAAAGTGTG CTTGGCATTGAAATAAAAGTTGGGGCTTATTTTCAATTCTCCCTGAAATTATT TCTTGACATTGACTAGCTCAGCAGTGTATCTAAATAAGCTTTTGGGTTCTATTATA [A, G] TAGAGGTTGTTCTTCTTCTCCCTTGAAAAGTATCATTGTCACATTATTGAAA ATCCAGGTGTTATATGATATTCTTATTGCCAGAGGGACATTCTGCAGGCTTTGTAAAA TGATTTTAGGATTTCAGATACTTATATATTATTGCCCCATAATTATCCAACTAG AAAATTAAACCTCTCTAAATCCATCTAAAGTGTGTAATTAAAGGAAACAC TAAAGATTCTTATTGGTGTCAAGAAACTCCTGTTCTACACAGTAGTATAAAACAAA
8866	ACATGTAACCAACAATGAAATTATTTAGTGAATTGAGAACTCAAAGTGTAGAGTTGA ATCCCTGTTCTACTACTTGCTAGCGGTGACCTGGGCTGTTAACCTTGACACCTT GTTTCCAAATTATAAAAGTGGAGATAATAATATCTGTACATTGTTGTTGAGGAT TATATGAACTAATATATGTAATGCTCTGAGAACAAATGTCGGTACACATTAAAGTAA AAATTAGCTGTTCTACTGTTATTATTAGACATGAGCTAGATAACAGTGGCTCTACATG [T, G] GAAAGATTATTTAATTCTGATGTAGTTCAGTTATCTATTGTTTATTGTCCTT TTGCATTGATGTCATATCTAAAAAACCTGCCTAACTCAGGATCACAAAAATTACTCCTG TATTTTATAATTAGCTCTTAGATCTAGGATCCATTAGCTAATTGTTATATATGG TGTGAGGTAGGGTACGGTTCATCTTGCACGTGAATAGCCAGTTGTCCCAGCATCA TTTATTCAAAGACTATTCTTCTCACTAGAAAAAATATTCTTAAAGAATAATGAAT
10397	CCAGGCTCCCTGAACCTGGGCTCAGATGATAGCCTCCTGCCACAGCGCTCTGATT AGCTGGACTACAGGTGTGACCAACTACACGTGGCTTCTGATGAAATTAAATACCC AAATATTGAGCAGAAATAATAGCTTGTGTTATTGTTTCTACTATCTGTCAAGTATA GTATTAAATGTTTACATAATTGTCCTCCAGTCCACATACAATACTCTAGTAGAAGTGG TAACAAAACCAAGGTACTCAAAGAGGTTAATAAGTAACCTGCCTGGATCACAGAACTAA [C, T] GGGAGGCAGGGCTGGAATTGACTCTAGGTCTTCTGACCTCAAAGTGCAGTAAAGTCAT GGAATTCTCTACTAGGCCACCTGGAAGAAAAGTGTATCTTTCCAGTCTTTGTTA CTGTTTCTAGCCAGGAGATAGTAGAGTTAGGTAGTAAAGTAGTACTGGCATTCCGG TAGTCAGCCCTCCAAAAAGTTGATTTTTTTTGCTTAAACTGGAG CTACTAACCTTCAGGTCACTCTTCTATCATCCAAGAGCTGGATATTAGGTAGCAGAA
10621	CTCTAGTAGAAGTGGTAACAAACCAAGGTACTCAAAGAGGTTAATAAGTAACCTGC GC

	TGGATCACAGAACTAACGGGAGGCAGGGCTGGAATTGACTCTAGGTCTTCTGACCTCA AAAGTCAGTAAAGTCATGGAATTCTACTAGGCCACCTGGAAGAAAAGTGTACTTTTT TCCAGTCTTTTGTACTGTTCTAGGCCAGGAGATAGTAGAGTTAGGTAGTAGAATAG TAGTCACTGGCATCCGGTAGTCAGCCCTCCAAAAAGTTTGTATTTTTTTTT [T, -] GTCTTAAACTTGAAGCTACTAACCTCAGGTCAACTTCTTATCATCCAAGAGCTGGA TATTAGGTAGCAGAAACTATGGAATTATCCTAAGTCCTTGTAGGCTTCAGCTGTTAA ATTAATTGGTTCTGATTAACACTGTGCTCAAGATTTACATTCTAGGAGGCCAGTTGA TTGGCTAACTGGATCTATGTTCTTAGCTGGGAGGAGAAGGTATCTGATTGA TACCTCACCGAGACTGCATGCAGTGAGGGACAGAAGTTCTAAAATAATTGGTTCT
19651	TTTATTTCTGCTACTATGGCAGAATTGAGTTGTCAGTGTGGCATCCAAAGCCTA AAATATTTACTCTCCTGGCTTTGCCAACCGTTAGATTATGAGCACTTGGCATTA TTATGTTTGTCTTCTATAGCACACAGTAAGATGTTGCCCACATTGTCATAA TTTATGGGTTTATTCAAGGATTATGCAAGTGTAGCTGCAAGAAAAAAACCTAGAAGTGA ACTTGCTAGGTTGAAGAGCA [A, G, T] CTGTGTATGTTAAATTTGTTAGCTTCCGCTTCCAAAGGGATTATTCCATTCTACT TAAACACTAAATTTGTGATAGGACTCTTCTCCATAGCTTGCTAAATTAAATGCATT ACACACTTCATCTTACTAACTGATAGAGGGAAATGATATTGTTGAGCTTGCATT TCTTTTATGTTAGCTGAGCTTATTTCATATTAAAAGCCAATTGTATTCTTTT CTTGAGCTATCTTTAATGT
19891	TTTATGCAAGTGTAGCTGCAAGAAAAAAACCTAGAAGTGAACCTGCTAGGTTGAAGAGCA TCTGTGTATGTTAAATTTGTTAGCTTCCGCTTCCAAAGGGATTATTCCATTCTACT TAAACACTAAATTTGTGATAGGACTCTTCTCCATAGCTTGCTAAATTAAATGCATT CACACACTTCATCTTACTAACTGATAGAGGGAAATGATATTGTTGAGCTTGCAT TTCTTTTATGTTAGCTGAGCTTATTTCATATTAAAAGCCAATTGTATTCTTT [T, -] CTTGAGCTATCTTTAATGTCCTTCTGATACATTCTGAAGTGTGATACTCATATAA GATATATGGTGAACATGTGTCAAAGATTATTGACTCTAAATGAGGGAACCCGCTGATG ACAAGGCTGATTGAGAAGAGGATGTTGAGATGAAGTGTATATCATCAGTGAAGAAAGC AAATTCTACAGGGCAAAACAAAACCACAACCTTAAGGTTATTGTTCTACTGGACAG AATTCAATTGCAATTACAGATAAAATTACTATTTCATTCTTACAAATCAT [C, A] AGGCTAATTGTTGACACTCGGGCTTGACTTTAAGAGAACATGCCATAATTCTTGGCCTT ACTTCCAAGTTGGATAATTCTTCTAACACATTCTCTAATTGCAATTGATTTCAAG TGATATTATTCTTTTTAAATTCTTACTATTGACTCTTGGGTGTTCT CGGAGAGGGGATTGGCAGGGTCATAGGACAATAGTGGAGGGAGGTCAAGCAGATAAAC ATGTGAACAAAGGTCTGGTTCTAGGCAGAGGACCCCTGGCCTCCACAGTGT
20272	CAAAGATTATTGACTCTAATGAGGGAACCCGCTGATGACAAGGCTGATTGAGAAGAG GATGTGTGAGATGAAGTGTATATCATCAGTGAAGAAAGCAAATTCTACAGGGCAAAA CAAAACCACAACTCTAAGGGTATTGTTCTACTGGACAGAACATTGCAATTGCAATT GATAAAAATTACTATTTCATTATCTTACAAATCTTCTAATTACAGAGTCT ATTCCCTAACAGTAGTAAATAGTCTCTAAATTCTCCGAGCAGTCAGGTGACTATTATG [C, A] AGGCTAATTGTTGACACTCGGGCTTGACTTTAAGAGAACATGCCATAATTCTTGGCCTT ACTTCCAAGTTGGATAATTCTTCTAACACATTCTCTAATTGCAATTGATTTCAAG TGATATTATTCTTTTTAAATTCTTACTATTGACTCTTGGGTGTTCT CGGAGAGGGGATTGGCAGGGTCATAGGACAATAGTGGAGGGAGGTCAAGCAGATAAAC ATGTGAACAAAGGTCTGGTTCTAGGCAGAGGACCCCTGGCCTCCACAGTGT
20412	TTATTGTTCTACTGGACAGAACATTGCAATTACAGATAAAAATTACTATTTC ATTATCTTTACAAATCATTTCTAATTACAGAGTCTATTCCCTAACAGTAGTAA TAGTCTTCAAAATTCTCCGAGCGTCAGGTGACTATTGCAAGGCTAATTGTTGACACTC GGGCTGACTTTAAAGAGAACATGCCATAATTCTTGGCCTACTTCAAGTTGGATAA TTTTCTTAACACATTCTCTAACAGTGTGATATTCAAGTGTAACTTCTT [T, A] AAATTTTTTACTATTGACTCTTGGGTGTTCTCGGAGAGGGGATTGGCAG GGTCATAGGACAATAGTGGAGGGAGGTCAAGCAGATAAACATGTGAACAAAGGTCTGG TTTCTTAGGCAGAGGACCTGCGGCCTCCACAGTGTGTCCTGGGTACTTGAGA TTAGGGAGTGGTGTGACTCTTAATGAGCATGCTGCTTCAAGCATCTGTTAACAAAGC ACATCTGCACCCCTTAATCCCTTAACCCCTGAGTTGACATAGCACATGTTCAGAGA
23340	TTTTTTTTGGAGGTGGGGACTGTGCCCCATTGTCATGGCCAAACTGGAGTGCAGTG GTGCAATCTGGCTCACTGCAACCTCTGCCCTCCAGGTTCAAGCGATTCTTGACTCAGC CTCCCTGAGTAGCTGGAATTAGGTGTGTCCTAGCAGTGTGCTCAGACTCCTGGCCTCAAGTGA AGTAGAGATGAAGTTGCGCATGTTGGCAGGGCTAGTCTCAGACTCCTGGCCTCAAGTGA

	TTGGCTGACCTCAGCCTCCAAAGTAGAAAATCTTCTGAAAAATAAAATTCAAATCTC [A, G]
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29948	GACTCTACCAATGGGATCGGAGCTCTCCAAACCTGCATATTAAAAGGCCTATAAGTTTG GGGGTCCCTTGTCCACATGATTCTGTAAATACATTGTATTGACATGGTATT TTATACACAGATCCTGCTTTAAAGAACATTATAATCCACTTAACGTGCTAGGACAGAG AATGACCGATAATTCAACCATATTGTCTACAGAAGACATATATAAAAGATGGTATGT GTACCAATTGAGGTCAAATTGATTCAATTAAAACAATCTAGGCCAGATTTATAG [T, A] TTGTGGACCCCTTGCACTCAAATCTCAAGGTTCTTATTAAAATGCAGATCTGGCTGGC ACGGTGGCTCACACCTGAATCCCAGCACTTGGGAGCCAAGGCAGGTAGATCATTGA GCTCAGAAGTTCAAGACCAGTCTGGCCAACATAGCGAGGGCCAGTCTCATTGAAAGAAAA AAAATTTTAATAAAAAATAAAAGCAGATCTGGTAAAGACATGTAGTCTGGTTACA GGTATTAACAACGTCTGTAATGTAGTGATTTGCTCCAGACTACCTTTCCATTATT
33579	TTACTGTGAAGGCTGATTTTTCTCTCACCACTAATTAAACACATGACTAGGCCAA TTTCAGACTATTAGTTAAACATCAAGAGCCTGGAAGAAGTATCTTGACCTAATGTT CTTGACGGGTTAGTTGTTACTTGTGTTATGACCTGAATTTTTTGAGACTG AGTCTTGCTGTCGCCCAGACTGGAGTGCAGTGGCGAATCTCAGCTCACTGCAACCTC TGCGTCCCAGGCTCAAGCAATTCTGTGTCAGCCTCTGAGGAGTTGCAGGC [A, C] CCTGTACCATGCCCTGCTAATTTCGATTTTGTTTTTTAGTAGAG ATGGGGTTTCACCATGTTGCCAGGCTGGCTCAAACCTCAAGTGTACCCCG CCTCAGCCTCCAAAGTGCCTGGGATTACAGGTTGAGGCCACACGTGGCTATGACCT GATTTGATTCACTTACTTTATAATTACCTTTGATTAGATAAGTTAATTCTTG ATTTGGCCATTATGCTTGAGAAAGTAGTTAATCACAGTGGTCAACAGTACAAACTT
40762	ATCCATCACCTCAAGCATTTCCTGTGTTACAAACAATCCAATTACACTCTTAATTA TTTTAAGTGTACAATTAAATTATTGAATATAGTTCAAAGACTTCTTCATTGACTAG CACCTAGGCTAAAAAAATTCAAGACACCTGGGCTCCTGGGATCAATCACGCATACTGTGTC TCTTGCTCACTCCC [G, A] CTGTCTCTCTCTTTCTCTCGCTCCTTTCTCTCTGTGGTTCTAGGGTGG TGGCCTAGGGATTGGATTCTTATATTAGTCACTCAGGATTCCAAGAGGGCTTTTT AATGTAGCCAAGAAGTCTGCAGCGTGAATTGTTATTCTATTGAGGTAGTCAC AGAGGCCGACCACAT
40936	TACAATTAAATTATTGAATATAGTCAAAGACTTCTCATTGACTAGCACCTAGGCT AAAAAAATTCAAGACACCTGGGCTCTGGGATCAATCACGCATACTGTGCTCTTGCTC ACTCCCGCTGTCCTCTCTCTCTCGCTCCTTTCTCTCTGTGGTTCT AGGGTGGTGGCCTCAGGAATTGGATTCTTATATTAGTCACTCAGGATTCCAAGAGGGC TGTTTTAATGTAGCCAAGAAGTCTGCAGCGTGAATTGTTATTCTATTGAGG [T, C] AGTCACAGAGGCCGACCACATTAGAGGAGGGACATACACTGCTGGACAAGTGTAG AGAATTGATGATCATGTTAAACCACTTTATTAGTTCTATTGCTGCTGTAAATAA TTACCCACAATTGCTTAAAGCCACACAAATTAAATCTACAGTCTGCAAATC AAAAGTCTGAAACGGATCTCACTGTGCTAAATTAGGTGTTAGGGCATTCTGGAGG CTGTAGGAGAGTAGTGTGTTTTGCTTCTGGTATTAAAGCTGCCAGCATTCTT
45998	TGTATATCAGTCAAAATTGGCAACTCTGATAAGTTGTCACCTAACATTGACCAC TTAAGATGAATAGCATCTACCATTCCGTATTGAAATATATAGGAGGACATAATCAC ATAATCTGAAAGTAAAGACAGTGTCTAAACTGAATCAGTTAAGTTATGAAAATAC TTCATATTGTAATTAAATTATATTGTTAATTCATAGCTTTGGGTTACAAGT GGTTTGTTACGTGGATGAATTCTATAATGGTAAGTCTAAGATTACTGCAACTGTC [A, G] CCCAAGTAGTATATATTGTATCCAGCATATTGCTCTTTTTCTTTTTCTTTTCA TTTCACCATGGACTAATGAAAATTGTTAGGGACTGACATTAGGGCACCCCTGAGCTAC CTTGAGCTAAAGGAAATAACCCCTGAAATTCTGTTGGCCTAGAGAATGTGGTTG

47771	TTTTGTAACATGGGATTGTTAAGGTACAAGATTTGCTTAGTTATTGCTA CTAGGATTTGCTATATTAAATACAATGTGAAAAGAATCAAAAGTGTAGAAATAATGCA GAAGAGTAGAACATGAGGCTTATTAAAAGATTAGCAGAATTAAAGGAAAAGGTGACTT TGTGAAAGATTATAATGTGAAGACAAAGGAACGAGGATGGAAATAAATTGTTGATTGAT AGGCTTGAGAAATTGACTCTAGAGAGTATATTGGGTACTTTGGAAATGAAGTTG GATTAGTGAGAAGGAACAGATTATGAAAAGACAAGAACCTGATTAATGTCAGGATGATT TTATATTGAG [T, C] TGGTCAGATTATGGCAGTCCTGGCTTGCCATTAGTTGATGACTTGAGAAAAGTT CCTTCTTGAAGTTAATTTCTGTATATAAAAAGTAATAACACCTGGTGTCTGCTAGG TTGTTTGAGGATTATATGAGATAAAATGCATGCAAAACTGTTATAATAGTGCCTGGTAA AAATAAGTGCCTAGTTAAAACAAGTCTTGTAAACTGCTTAGGACATGCCTGGTATA GGTAGGTATGT
48117	GACTTTGAGAAAGTCCCTCTGAGTTAATTCTGTATATAAAAAGTAATAACACC TGGTGATCTGCTAGGTTGAGGATTATATGAGATAAAATGCATGCAAAACTGTTA TAATAGTGCCTGGTAAAATAAGTGCCTAGTTAAAACAAGTCTTGTAACACTGCTTAG GACATGCCTGGTATAGGGTAGGTATGTAATACATAGTAGGTAGGATCTGTCCTTGCTA TTTTAGGTAAAAAAACAAAGGAAGAGCAGCTCAGCTTAATACAGTATGAACTGACGAGCC [C, T] TGGTAGGTTTGAGCAAAGAGCAACACAGTAAAAGTAGTACTTAGGAAAGATTAACAA GGAAACATGGCTTATACAGTGTAAATGGGGCTGGAGTCAGGAGGTAAAGATAAAATGGT ATTATAATTAAGGAATAGCCAGGCACGATGGCACATGCATGTAATGCCAGTACTGGAGA GGCTGAGGTGGGAGGATCATGGAGTCCAGGAGTTGAGACAGCAGCTGGCAACTGAGT AGACCCCCAATCTAAAAATACAAAGTAAAAAGGAATAAAAGTCACTGAGGGCTTGGACT
54563	GCTTGTACCCAGGCTGGAGTGTGGTGTATGATCATGGCTGACTGCGAGCCCTGACCTT CCGGGCTCAAGTGTATTTCCACCTCAGCCTCCAAATTACTGGGACCAACAGCATGCTT GGCCGATTTTTTTTTTTTTTTGTAGAAGCAAGGTTCCCTATGTTGCCAGGCG TGGTCTTGAACTTAGGGCTATGTGATACCTCTGCCCTGGCCCTCCAAAGTGTAGGAT TACAAGCCTGAGCCACCATGGCGGCCAAATATTTCACTATAACAAATATCATATCTG [T, G] ATATAACTCAGTTAATACTAACTCAAAGTAGAAACATAAGCTGATGACTATTATT TTCAGATTCTCTCATTGAGTTCCCTCTCGTCTGTGATCTGACTTTCTCCA TCTTGCCACTTCTGTCTAGCATTTTTATCAGACTTCACTCAGATTCTGAGTTTTTT TTAGTTCTTCAACGGTGGAGTGGAGTAGGCAGCAGGACAGAACTGAGCAGAGC ACACTGGAGAGGAGAAATTACAAAGCCTTATGAAATAAAACACCCCCAATATCAGTC
58735	TGGGTTATGCCCTGTTAATCTACATCATTAGTTAGCCAAAAGGAAACAGCAAAT AAATGTTTATATGAGCCACATTGCGTTGATTTCTTCCACTCTGTAAGAAATTACTAA GCAGCACTCTGACTTTATTATGCTCAAATCGCTCTCCATTATGTTGTTCTCCAT CTTTAGGGTTTACTTTATAAAATACAGAGATTACTGTTGAAATTCTAAATTGCCAC TGGGCGTTATACATTGTAACCTCCTCACAGTATATTGTTGATTTGGCAGAGTTAC [C, T] AAATAGATGATACTAACTGAAATTAACTCATTCTGTATAATTGGAGTAGAAAGCATGAGT AAGAATTCAATTGGTATTATTTAATTAATTGCAAGATTTCAATTCTGACTACA ACAATAAAATCAAATGAATTGATGGCTAAAAAGAAATCTAAATGTTAGTCAGT AAGAACATCTATTGAATGAGTGAATGTTCTATTATATAGTGCATTCTGAGCTTTTT GGAGGGGGAGTTGCTCCATGCTCTGAGAACATTAAAGGATCGATACATTATTTTAAC
59643	GTTCATATTGCCACATTAATTCCATTATAAAACCAGTAACCATAGTTGTTTAATT GCAATCTAATTATTTCATGTATCCTCATATGAGAAATTATGTCCTACATTGCTG TGTGATAACAGTGACATGCTAAATGAGAAACAAATTGTTGAGGAAAGGAAATGCA TGAAAGTCTTTAATCCCTAATCATAAAACATTTATTAGCTACTTTAAGAAGTGGC AGTCACAGCTCCTGAACATTAGGGAGTGTCTGGTCACTTAAAGGATCGATACATT [C, A] ATTGCCTTAATTAAATTGAAATTATAGTAAACATGCCACGGGAGTTTTAAGTCTCCTC ACAGCCTTGTCTACCTTCAACCAAGGTAGATCCAGATGATAACTGCTGTGAGCA TCATAGAAATTAGAAAAATATTTCCTGAGGAAAGAACATTGTAATGAAACACTCTACA TATCAGAGGTCTAGCTATGTATCAATATTAAAGTTCTTTGTTACTTGTAGTC ATCTTCATTCAAACATTCTATAATTATTATTAAAGTAAAGAAAATAACCCACCA

61638 AAAAAAAGGAAAACATTGATAAGTGTCCCTAGAAACTGGATTCTTATAGATTTGTCT
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 [G, T]
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 [G, C]
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63463 TGTGCCGTGGCTCAAAACGAAAACAATGAAGCTGGTTAAAGGATAAAAGTTCT
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 [A, G]
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63636 TGCTGCTGCTTGACAGTAAAGAGAAGGAAGTATTCTGATTAGCTGTATCTGGTATTAAT
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 [G, A]
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 [T, C]
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